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FIGURE 1

[SEQ.ID.NO.:5] Nucleic Acid sequence of the human 5-HT3-C (full sequence including untranslated regions); 1745 bases. (34 bases of 5' UTR; 367 bases of 3' UTR)

TGGTGAATCCCCAGAGAAGAGTCCAGAAAGAAGAATGGAAGGAGGGTGGCCTGCAAGGCAGAGTGCCCT
CCTCTGCCTCACTGTCAGTCTTCTGCTTCAAGGAAGAGGCGACGCTTTTACCATCAATTGCTCAGGCTT
TGACCAGCATGGGGTTGACCCTGCTGTCTTCCAAGCAGTGTTTGACAGAAAGGCCTTCCGTCCATTAC
CAACTACAGCATCCCTACCCGTGTCAACATCTCCTTCACCCTGTCTGCCATCCTGGGAGTGGATGCACA
GCTCCAGCTGCTGACATCATTCTGTGGATGGATTGTTGATATGGGACAATCCTTTCATTAATTGGAACCC
AAAAGAGTGTGTTGGCATCAATAAACTCACAGTATTAGCTGAAAACCTGTGGCTCCCAGACATCTTCAT
CGTGGGAATCCATGGATGTGGATCAGACGCTTCCGGTCTCACTGCCTATATCAGCAGTGAAGGTGGAAT
TAAGTATGATAAGCCAATGAGGGTGACCAGCATCTGTAACTGGACATCTTCTACTTCCCTTTTGACCA
ACAGAACTGTACCTTCACCTTCAGTTCTTTCCTCTACACAGTGGACAGCATGCTGCTGGGCATGGACAA
GGAGGTGTGGGAGATCACAGACACGTCTCGCAAAGTCATCAAACCCAGGGGGAGTGGGAGCTCTTGGG
CATCAACAAGGCCACCCCAAAGATGTCCATGGGCAACAACCTATATGACCAGATCATGTTTTATGTGGC
CATCAGGCGCAGGCCAAGCCTCTACATCATAAACCTGCTGGTGCCAGTAGCTTTCTGGTTGCCATTGA
TGCCCTCAGCTTCTACCTGCCAGCAGAGAGCGAGAATCGTGCCCCATTCAAGATAACACTTCTGCTGGG
CTACAACGCTTCTCTGCTCATGATGAATGACTTGCTCCCTGCCAGTGGCACCCCCCTCATCAGTGTCTA
CTTCGCCCTGTGCCTGTCCCTGATGGTGGTCAGCCTGCTGGAGACCGTCTTCATTACCTACCTGCTGCA
CGTGGCCACCACCCAGCCCCACCCATGCCTAGGTGGCTTCACTCCCTGCTGCTCCACTGCACCAGCCC
AGGGAGATGCTGTCCCACTGCGCCCCAGAAGGGAAATAAGGGCCTGGGTCTCACCTCACCCACCTGCC
TGGCCCAAAGGAGCCGGGGAGTTAGCAGGGAAGAAGCTGGGACCCAGAGAGACCGAGCCAGATGGGGG
CTCAGCATGGACAAAGACCCAGCTAATGGAGCTGTGGGTGCAGTTCAGCCACGCGATGGACACCCTGCT
CTTCGCGCTCTACCTGCTCTTCATGGCCTCCTCCATCCTTACTGTCAATTGTCCTCTGGAACACCTAGGC
AGACATCCCCCTCTCTGGCAAACAACAGCTTGGAGTTTCTGCTGGTCTTGGGCCAGCCGGACTCATTT
TCCTAATCTTAGCCACTTATCCCCAGTGAATACCATGTCCCCTTCTAAATTCCAAAGAATCCAACGCAG
CACTAGCAAGCAGGTTTCAAGACAGCCCTGGACGATTTCCCGACCGCTGCTCAGGGTGGTCATTCTGCT
CACCTCAGTTTCCCTGAGGTACCACCTAACTCCTCACTCCCTGATCAATGGAAGTTTCAAGTCAAGTGA
GTCTTTCCTTGATTGATCACCCCAATAAACAACCTTTTCAGGGAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAA

FIGURE 2

[SEQ.ID.NO.:6] Nucleotide sequence for the coding region of 5-HT3-C is shown; 1341 [this does not include the TAG termination codon] bases.

ATGGAAGGAGGGTGGCCTGCAAGGCAGAGTGCCCTCCTCTGCCTCACTGTCAGTCTT
CTGCTTCAAGGAAGAGGGCGACGCTTTTACCATCAATTGCTCAGGCTTTGACCAGCAT
GGGGTTGACCCTGCTGTCTTCCAAGCAGTGTTTGACAGAAAGGCCTTCCGTCCATTC
ACCAACTACAGCATCCCTACCCGTGTCAACATCTCCTTCACCCTGTCTGCCATCCTG
GGAGTGGATGCACAGCTCCAGCTGCTGACATCATTCTGTGGATGGATTTGGTATGG
GACAATCCTTTTATTAATTGGAACCCAAAAGAGTGTTGGCATCAATAAACTCACA
GTATTAGCTGAAAACCTGTGGCTCCCAGACATCTTCATCGTGGAATCCATGGATGTG
GATCAGACGCCTTCCGGTCTCACTGCCTATATCAGCAGTGAAGGTCGAATTAAGTAT
GATAAGCCAATGAGGGTGACCAGCATCTGTAACTGGACATCTTCTACTTCCCTTTT
GACCAACAGAACTGTACCTTCACCTTCAGTTCTTTCTCTACACAGTGGACAGCATG
CTGCTGGGCATGGACAAGGAGGTGTGGGAGATCACAGACACGTCTCGCAAAGTCATC
CAAACCCAGGGGGAGTGGGAGCTCTTGGGCATCAACAAGGCCACCCCAAAGATGTCC
ATGGGCAACAACCTATATGACCAGATCATGTTTTATGTGGCCATCAGGCGCAGGCCA
AGCCTCTACATCATAAACCTGCTGGTGCCAGTAGCTTTCTGGTTGCCATTGATGCC
CTCAGCTTCTACCTGCCAGCAGAGAGCGAGAATCGTGCCCCATTCAAGATAACACTT
CTGCTGGGCTACAACGTCTTCCTGCTCATGATGAATGACTTGCTCCCTGCCAGTGGC
ACCCCCCTCATCAGTGTCTACTTCGCCCTGTGCCTGTCCCTGATGGTGGTCAGCCTG
CTGGAGACCGTCTTCATTACCTACCTGCTGCACGTGGCCACCACCCAGCCCCACCC
ATGCCTAGGTGGCTTCACTCCCTGCTGCTCCACTGCACCAGCCCAGGGAGATGCTGT
CCCCTGCGCCCCAGAAGGGAAATAAGGGCCTGGGTCTCACCTCACCCACCTGCCT
GGCCCAAAGGAGCCGGGGGAGTTAGCAGGGAAGAAGCTGGGACCCAGAGAGACCGAG
CCAGATGGGGGCTCAGGATGGACAAAGACCCAGCTAATGGAGCTGTGGGTGCAGTTC
AGCCACGCGATGGACACCCTGCTCTTCGCCTCTACCTGCTCTTCATGGCCTCCTCC
ATCCTTACTGTCATTGTCCTCTGGAACACCTAG

FIGURE 3

[SEQ.ID.NO.:9] The amino acid sequence of 5-HT3-C is shown (447 amino acids).

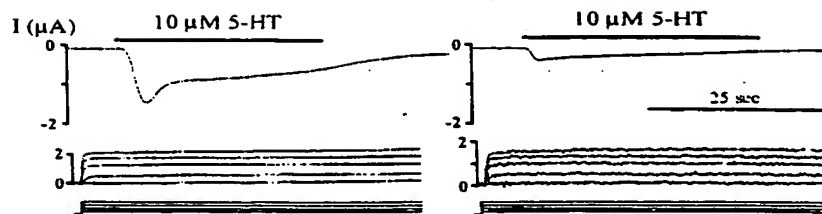
MEGGWPARQS ALLCLTVSLL LQGRGDAFTI NCSGFDQHGVDPAVFQAVFD
RKAFRPFTNY SIPTRVNISF TLSAILGVDA QLQLLTSFLW MDLVWDNPF
NWNPKCEVGI NKLTVLAENL WLPDIFIVES MDVDQTPSGL TAYISSEGR
KYDKPMRVTS ICNLDIFYFP FDQQNCTFTF SSFLYTVDSM LLGMDKEVWE
ITDTSRKVIQ TQGEWELLGI NKATPKMSMG NNLYDQIMFY VAIRRRPSLY
IINLLVPSSF LVAIDALSFY LPAESENRAP FKITLLLGYN VFLMMNDLL
PASGTPLISV YFALCLSLMV VSLLETVFIT YLLHVATTQP PPMRWLHSL
LLHCTSPGRC CPTAPQKGNK GLGLTLTHLP GPKEPGELAG KKLGPTEP
DGGSGWTKTQ LMELWVQFSH AMDTLLFRLY LLFMASILT VIVLWNT

MEGGWPARQS
ALLCLTVSLL
LQGRGDAFTI
NCSGFDQHGVD
PAVFQAVFD
RKAFRPFTNY
SIPTRVNISF
TLSAILGVDA
QLQLLTSFLW
MDLVWDNPF
NWNPKCEVGI
NKLTVLAENL
WLPDIFIVES
MDVDQTPSGL
TAYISSEGR
KYDKPMRVTS
ICNLDIFYFP
FDQQNCTFTF
SSFLYTVDSM
LLGMDKEVWE
ITDTSRKVIQ
TQGEWELLGI
NKATPKMSMG
NNLYDQIMFY
VAIRRRPSLY
IINLLVPSSF
LVAIDALSFY
LPAESENRAP
FKITLLLGYN
VFLMMNDLL
PASGTPLISV
YFALCLSLMV
VSLLETVFIT
YLLHVATTQP
PPMRWLHSL
LLHCTSPGRC
CPTAPQKGNK
GLGLTLTHLP
GPKEPGELAG
KKLGPTEP
DGGSGWTKTQ
LMELWVQFSH
AMDTLLFRLY
LLFMASILT
VIVLWNT

FIGURE 4.

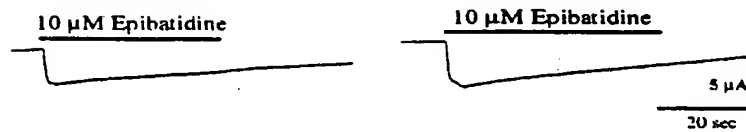
**5-HT_{3A(short)}
receptors**

A.



B.

**α 3 β 4 nicotinic
ACh receptors**

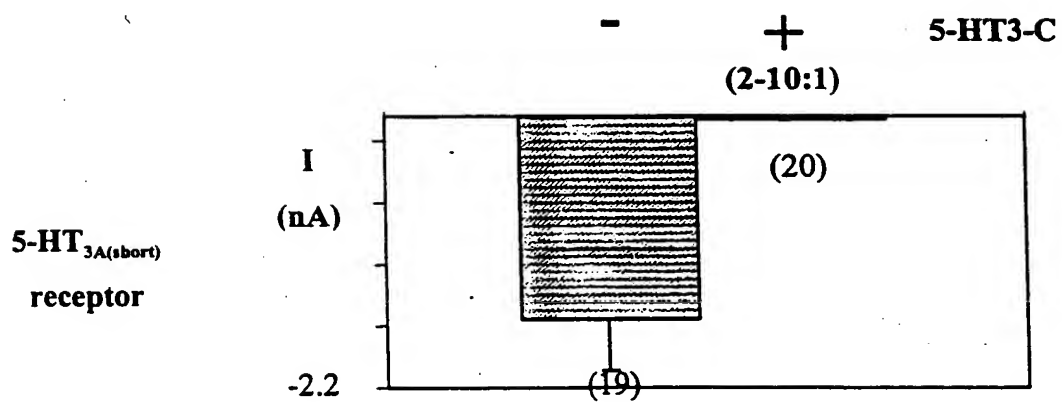


Shaker/H₂O

Shaker/5-HT3-C

FIGURE 5.

A



B

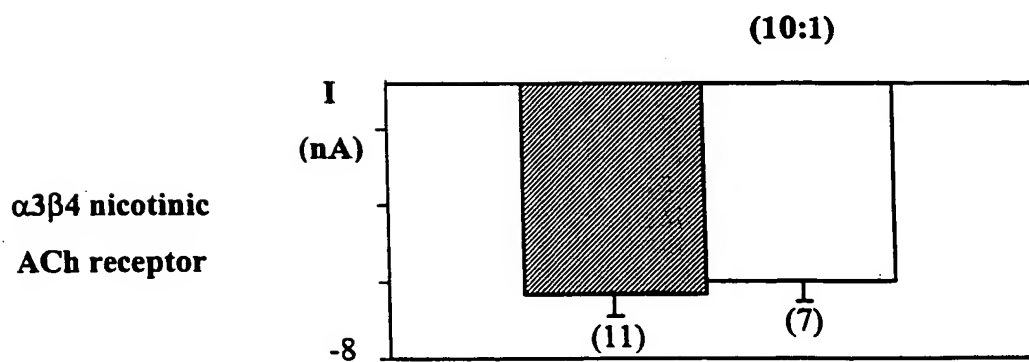


FIGURE 6

Figure 6a.

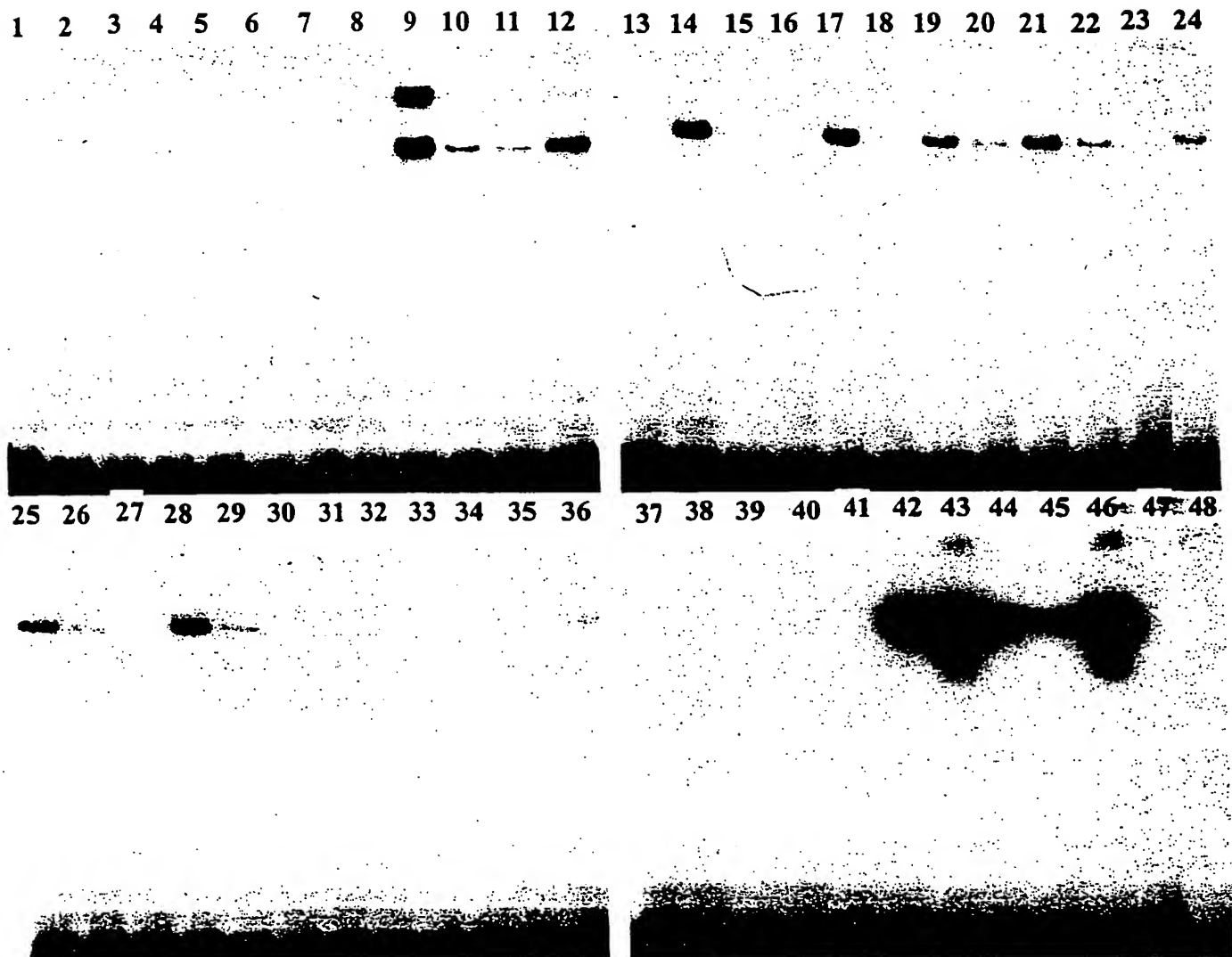


Figure 6b.

Tissue or cell type	5-HT _{3C} (mean intensity)	5-HT _{3A} (mean intensity)
CD19+ B-cells	501 +/- 42 (p < 0.005)	66 +/- 10 (p<0.025)
Fibroblasts	142 +/- 37 (p < 0.025)	84 +/- 5 (p < 0.0005)
DRG	110 +/- 10 (p< 0.01)	140 +/- 10 (p < 0.0005)
Mammary gland	102 +/- 13 (p< 0.0025)	96 +/- 16 (p < 0.01)
Salivary gland	96 +/- 4 (p < 0.0005)	98 +/- 11 (p < 0.005)
Bone marrow	94 +/- 3 (p < 0.0005)	74 +/- 13 (p < 0.05)
Liver	93 +/- 5 (p < 0.0005)	NS
Small airway epithelial cells	92 +/-14 (p < 0.025)	NS
Stomach antrum	90 +/- 5 (p < 0.001)	110 +/- 40 (NS)
Olfactory bulb	89 +/- 7 (p < 0.05)	91 +/- 13 (NS)
Prostate	86 +/- 7 (p < 0.0025)	66 +/- 4 (p < 0.01)
Whole blood	82 +/- 4 (p < 0.0005)	50 +/- 10 (p < 0.05)
Thymus	79 +/- 6 (p < 0.0005)	56 +/- 4 (p < 0.0025)
Placenta	78 +/- 11 (p < 0.01)	53 +/- 4 (p < 0.025)
Small intestine	78 +/- 3 (p < 0.0005)	82 +/- 8 (p < 0.005)
Adrenal gland	75 +/- 5 (p < 0.001)	NS
Pancreas	74 +/- 4 (p < 0.001)	125 +/- 34 (p < 0.05)
Lymph node	74 +/- 7 (p < 0.001)	NS
Gallbladder	74 +/- 10 (p < 0.001)	NS
Thyroid	73 +/- 8 (p < 0.025)	57 +/- 4 (p < 0.05)
Uterus	72 +/- 3 (p < 0.0005)	55 +/- 6 (p < 0.05)
Testis	70 +/- 4 (p < 0.0005)	56 +/- 4 (p < 0.01)
Hypothalamus	69 +/- 10 (p < 0.025)	80 +/- 12 (p < 0.05)

Tissue or cell type	5-HT _{3C} (mean intensity)	5-HT _{3A} (mean intensity)
Substantia nigra	67 +/- 5 (p < 0.025)	NS
Amygdala	65 +/- 6 (p < 0.05)	*
Bronchial smooth muscle cells	46 +/- 3 (< 0.005)	NS
Trachea	40 +/- 2 (p < 0.005)	85 +/- 16 (p < 0.025)
<p>Values are the mean intensity of the labeled cRNA hybridizing to the cDNA microarray +/- S.E.M. The mean intensity for cRNAs from all tissues shown were significantly different (p value in parentheses) from 75% of the control-plant cDNA value. Data are averaged from 3-6 experiments. * 5-HT₃-A receptor subunit is expressed in these tissues but at low abundance (Bufton et al., 1993; Sugita et al., 1992). NS= not significant.</p>		